

SEQUENCE LISTING

<110> Outtrup, Helle
Pedersen, Poul
Sorensen, Marianne

<120> Subtilase Enzymes

<130> 10065.200-US

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 1143

<212> DNA

<213> Bacillus clausii

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att tct	gtc gct	ttt agt	tca tcg	att gca	tcg gct	gct gaa	gaa gca	93
Ile Ser	Val Ala	Phe Ser	Ser Ser	Ile Ala	Ser Ala	Ala Glu	Glu Ala	
-95		-90			-85			

aaa gaa	aaa tac	tta att	ggc ttt	aat gaa	cag gaa	gct gtc	agt gag	141
Lys Glu	Lys Tyr	Leu Ile	Gly Phe	Asn Glu	Gln Glu	Ala Val	Ser Glu	
-80		-75		-70		-65		

ttt gtc	gaa caa	gta gat	gca aat	aat gat	gtc gcc	gtt ctc	tct gag	189
Phe Val	Glu Gln	Val Asp	Ala Asn	Asn Asp	Val Ala	Val Leu	Ser Glu	
	-60		-55			-50		

gaa gag	gaa gtc	gaa att	gaa ctg	ctt cat	gag ttc	gaa acc	att ccc	237
Glu Glu	Glu Val	Glu Ile	Glu Leu	Leu His	Glu Phe	Glu Thr	Ile Pro	
	-45		-40		-35			

gtt tta	tca gta	gag tta	agc cca	gaa gat	gtg gat	acg ctt	gaa ctc	285
Val Leu	Ser Val	Glu Leu	Ser Pro	Glu Asp	Val Asp	Thr Leu	Glu Leu	
	-30		-25		-20			

gat cca	gcg att	tct tac	att gag	gaa gat	gta gaa	gta tcg	att atg	333
Asp Pro	Ala Ile	Ser Tyr	Ile Glu	Glu Asp	Val Glu	Val Ser	Ile Met	

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cat aac cgc gga gtg aca ggt tcc ggt gta aaa gtt gct gtt ctt gat His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp 20 25 30	429			
aca ggc att tcc gcc cat cca gac tta aat atc cgc ggc ggt gct agc Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser 35 40 45	477			
ttt gtg aca ggc gag cca acg tat caa gat ggc aat gga cac ggc acg Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr 50 55 60	525			
cat gtg gca ggg acg att gcc gct tta aac aat tcg att ggc gtc ctt His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu 65 70 75 80	573			
ggc gta gcg cct aat gct gaa cta tac gct gtt aaa gta tta gca gcc Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala 85 90 95	621			
aac ggc aga ggc cca gtc agc tca att gcc caa ggc ttg gaa tgg gca Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala 100 105 110	669			
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cca agc gca acg ctt gag caa gcg gtt aat agc gct act tct aga ggc Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly 130 135 140	765			
gtc ctt gtc gta gca gca act gga aac tca gga aca ggc tcc ctc gac Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp 145 150 155 160	813			
tac cca gct cgt tat gcg aac gct atg gca gtc gga gct act gac caa Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln 165 170 175	861			
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gtt gcg cca ggt gta aac gtg cag agc aca tac cca ggt tca act tac Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr 195 200 205	957			
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gca gcc ctt gta aaa caa aaa aac cca tct tgg tcc aat gta caa atc 1053
 Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
 225 230 235 240

cgc aat cat cta aag aat aca gcc aca agt ttg ggt agc acg aac ttg 1101
 Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
 245 250 255

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Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
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Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
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Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
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Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
 -30 -25 -20

Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
 -15 -10 -5 -1

Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
 1 5 10 15

His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
 20 25 30

Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
 35 40 45

Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr
50 55 60

His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
65 70 75 80

Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala
85 90 95

Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100 105 110

Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115 120 125

Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130 135 140

Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp
145 150 155 160

Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165 170 175

Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180 185 190

Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195 200 205

Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val
210 215 220

Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225 230 235 240

Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245 250 255

Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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Ala Gly Gly Leu
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Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
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His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
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Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
35 40 45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala

130

135

140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145 150 155 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
165 170 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
245 250 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275